What is claimed is:

1. A method for the identification, isolation or separation of identical nucleic acid fragments from a mixture of at least two nucleic acid populations, comprising the steps of:

a) performing separate digestion of the nucleic acids from said at least two populations with at least one restriction enzyme;

b) ligating a differently composed adaptor molecule to the restriction fragments, wherein said adaptor molecule adds a distinct label for each of said at least two nucleic acid populations;

c) hybridizing said ligation products generated in step (b) with each other; and

d) identifying, isolating or separating the identical, fully matched, heterohybrid fragments.

2. The method of claim 1, wherein said nucleic acid populations are selected from the group consisting of genomic DNA populations, human genomic DNA populations, or populations comprising different subjects having a common trait of interest.

3. The method of claim 1, wherein said nucleic acid populations comprise a selected chromosome(s).

4. The method of claim 1, wherein two or more nucleic acid populations from different sources are used.

5. The method of claim 2, wherein two or more nucleic acid populations from different sources are used.

6. The method of claim 3, wherein two or more nucleic acid populations from different sources are used.

7. The method of claim 1, wherein the restriction fragments generated by step (a) are size selected prior to the amplification reaction.

8. The method of claim 1, wherein said adaptor molecule comprises a recognition site for *mut* HL.

9. The method of claim 8, wherein said adaptor molecule is in the range of about 5 to about 100 base long double-stranded DNA fragment comprising at least one GATC motif.

10. The method of claim 1, wherein said adaptor molecule is labelled by one or more selected from the group consisting of adding a unique end sequence to each adaptor, adding a chemical activity to the adaptor which provides a means to distinguish between the ligation products from different nucleic acid populations, or adding modified nucleotides into the adaptor allowing to distinguish between the ligation products from different nucleic acid populations.

11. The method of claim 1, wherein said identifying matched heterohybrids comprises the steps of:

(a) separating the homoduplexes from the heteroduplexes;

(b) identifying and eliminating the mismatched heterohybrids; and

c) identifying, isolating or separating the identical heterohybrid fragments.

12. The method of claim 11, wherein said heterohybrids are separated from said homohybrids based on labelling of said adaptor molecule.

13. The method of claim 12, wherein said heterohybrids are separated from said homohybrids comprising the steps of:

(a) performing a separate ligation of the restriction fragments with an adaptor molecule comprising a unique end sequence for each nucleic acid population;

(b) mixing the ligation products from the different nucleic acid populations carrying unique 5' ends;

(c) denaturating and rehybridizing said nucleic acids;

(d) digesting perfectly matched (blunt ended) DNAs (homoduplexes) by *Exo* III; and

(e) eliminating said *Exo* III created single strands by binding to a single strand specific matrix.

14. The method according to claim 13, wherein said adaptor molecules are non-complementary for at least about 4 nucleotides up to about 10 nucleotides at the ends in said heterohybrids.

15. The method of claim 11, wherein said mismatched heterohybrids are eliminated with mismatch repair enzymes.

16. The method of claim 15, wherein said mismatched nucleic acid fragments are eliminated by incubating the hybridization mixture produced in step (c) with MutS and contacting the resulting product with a *Mut*S-binding material.

17. The method of claim 15, wherein said mismatched nucleic acid fragments are eliminated by incubating the hybridization mixture produced in step (c) with *Mut*S, *Mut*L and *Mut*H, resulting in a specific cleavage of the mismatched hybrids.

18. A method of separating identical DNA fragments from complex mixtures of at least two nucleic acid populations, comprising the steps of:

hybridizing said at least two nucleic acid populations; and

separating the identical heterohybrids formed, wherein each said nucleic acid population is coupled to a differently labelled adaptor molecule.

19. A method to identify DNA regions that are relevant to a pathological condition or a particular trait, comprising the steps of:

hybridizing at least two nucleic acid populations from different sources having the particular trait or pathology; and

separating the identical heterohybrids formed which comprise DNA regions that are relevant to said pathological condition or said particular trait, wherein said nucleic acid populations comprise nucleic acids coupled to differently labelled adaptor molecules.